

WHAT IS CLAIMED IS:

1. A eukaryotic diploid multicellular parasite transformed with a transgene.
2. The parasite of claim 1, wherein the parasite is a worm.
3. The parasite of claim 2, wherein said worm is a flat worm.
4. The parasite of claim 3, wherein said flat worm is a trematode.
5. The parasite of claim 4, wherein said trematode is a schistosome.
6. The parasite of claim 1, wherein the parasite is infective to human or animal.
7. The parasite of claim 1, wherein the parasite is infective to human.
8. The parasite of claim 5, wherein said schistosome is infective to human.
9. The parasite of claim 5, wherein said schistosome is selected from the group consisting of *Schistosoma mansoni*, *Schistosoma haematobium*, *Schistosoma japonicum*, *Schistosoma bovis*, *Schistosoma mattheei*, *Schistosoma rhodhaini*, *Schistosoma magrebowiei*, *Schistosoma intercalatum*, *Schistosoma curasoni*, *Schistosoma mekongi*, *Schistosoma spindale*, *Schistosoma leipere*, *Schistosoma turkestanicum*, *Schistosoma inidicum*, *Schistosoma nasalis* and *Schistosoma suis*.
10. The parasite of claim 1, wherein the parasite is sterile.
11. The parasite of claim 1, wherein the parasite is sensitive to a known drug.

12. The parasite of claim 1, wherein said transgene is integrated in the parasite genome.

13. The parasite of claim 1, wherein said transgene is integrated in the parasite genome.

14. The parasite of claim 1, wherein said transgene is integrated in a selected genomic locus in the parasite genome.

15. The parasite of claim 14, wherein said selected genomic locus is a repetitive sequence.

16. The parasite of claim 14, wherein said selected genomic locus is a unique sequence.

17. The parasite of claim 1, wherein the parasite has distinguishable sexes.

18. A method of providing a eukaryotic host with a protein or polypeptide, the method comprising the step of infecting the eukaryotic host with a eukaryotic diploid parasite transformed with a polynucleotide sequence encoding the protein or polypeptide.

19. The method of claim 18, wherein said protein or polypeptide is secreted from said parasite.

20. The method of claim 18, wherein said infection is by a plurality of individuals of said parasite, all of said individuals are of a single sex.

21. The method of claim 20, wherein said single sex is selected from the group consisting of male and female.

22. The method of claim 18, wherein said parasite is a worm.

23. The method of claim 22, wherein said worm is a flat worm.

24. The method of claim 23, wherein said flat worm is a trematode.

25. The method of claim 24, wherein said trematode is a schistosome.

26. The method of claim 18, wherein said host is human or animal and said parasite is infective to said human or animal.

27. The method of claim 18, wherein said host is human and said parasite is infective to human.

28. The method of claim 25, wherein said schistosome is infective to human.

29. The method of claim 25, wherein said schistosome is selected from the group consisting of *Schistosoma mansoni*, *Schistosoma haematobium*, *Schistosoma japonicum*, *Schistosoma bovis*, *Schistosoma mattheei*, *Schistosoma rhodhaini*, *Schistosoma magrebowiei*, *Schistosoma intercalatum*, *Schistosoma curasoni*, *Schistosoma mekongi*, *Schistosoma spindale*, *Schistosoma leipere*, *Schistosoma turkestanicum*, *Schistosoma inidicum*, *Schistosoma nasalis* and *Schistosoma suis*.

30. The method of claim 18, wherein said parasite is sterile.

31. The method of claim 18, wherein said parasite is sensitive to a known drug, said drug is therefore effective in removing said parasite from said host.

32. The method of claim 18, wherein said polynucleotide sequence is integrated in said parasite's genome.

33. The method of claim 32, wherein said integration is by homologous recombination into a selected genomic locus.

34. The method of claim 33, wherein said selected genomic locus is a repetitive sequence.

35. The method of claim 33, wherein said selected genomic locus is a unique sequence.

36. The method of claim 18, wherein said parasite has distinguishable sexes, whereby a single sex of said sexes is used for said infection.

37. A method of genetically modifying a eukaryotic diploid parasite, the method comprising the step of transforming the eukaryotic diploid parasite using a group transformation method.

38. The method of claim 37, wherein the parasite is a worm.

39. The method of claim 38, wherein said worm is a flat worm.

40. The method of claim 39, wherein said flat worm is a trematode.

41. The method of claim 40, wherein said trematode is a schistosome.

42. The method of claim 37, wherein the parasite is infective to human or animal.

43. The method of claim 37, wherein the parasite is infective to human.

44. The method of claim 41, wherein said schistosome is infective to human.

45. The method of claim 41, wherein said schistosome is selected from the group consisting of *Schistosoma mansoni*, *Schistosoma haematobium*, *Schistosoma japonicum*, *Schistosoma bovis*, *Schistosoma mattheei*, *Schistosoma rhodhaini*, *Schistosoma magrebowiei*, *Schistosoma intercalatum*, *Schistosoma curasoni*, *Schistosoma mekongi*, *Schistosoma spindale*, *Schistosoma leipere*, *Schistosoma turkestanicum*, *Schistosoma inidicum*, *Schistosoma nasalis* and *Schistosoma suis*.

46. The method of claim 37, wherein the parasite is sensitive to a known drug.

47. The method of claim 37, wherein said group transformation method is selected from the group consisting of electroporation, chemical transformation, lipofection and biolistic bombardment.

48. The method of claim 37, wherein said transgene is integrated in the parasite genome.

49. The method of claim 37, wherein said transgene is integrated in a selected genomic locus in the parasite genome.

50. The method of claim 49, wherein said selected genomic locus is a repetitive sequence.

51. The method of claim 49, wherein said selected genomic locus is a unique sequence.

52. The method of claim 37, wherein the parasite has distinguishable sexes.